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APR 07

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RAW SEQUENCE LISTING   DATE: 04/02/2003
PATENT APPLICATION: US/10/017,372E TIME: 12:41:45

Input Set : A:\61302 Seq Listing.txt
Output Set: N:\CRF4\04022003\J017372E.raw

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 3 <110> APPLICANT: Wolfraim, Lawrence A
 4        Letterio, John J
 6 <120> TITLE OF INVENTION: FUNCTIONALIZED TGF-BETA FUSION PROTEINS
 8 <130> FILE REFERENCE: 4239-61302
10 <140> CURRENT APPLICATION NUMBER: US 10/017,372E
11 <141> CURRENT FILING DATE: 2001-10-19
13 <150> PRIOR APPLICATION NUMBER: US 60/242,292
14 <151> PRIOR FILING DATE: 2000-10-20
16 <160> NUMBER OF SEQ ID NOS: 39
18 <170> SOFTWARE: PatentIn version 3.2
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21 <211> LENGTH: 28
22 <212> TYPE: DNA
23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Primer
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57 <211> LENGTH: 45
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59 <213> ORGANISM: Artificial Sequence
61 <220> FEATURE:
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68 <210> SEQ ID NO: 5
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RAW SEQUENCE LISTING
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Input Set : A:\61302 Seq Listing.txt
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 73 <220> FEATURE:
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 83 <213> ORGANISM: Artificial Sequence
 85 <220> FEATURE:
 86 <223> OTHER INFORMATION: Primer
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 93 <211> LENGTH: 8
 94 <212> TYPE: PRT
 95 <213> ORGANISM: Artificial Sequence
 97 <220> FEATURE:
 98 <223> OTHER INFORMATION: Synthetic oligopeptide
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102 Asp Tyr Lys Asp Asp Asp Asp Lys
103 1               5
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107 <211> LENGTH: 1197
108 <212> TYPE: DNA
109 <213> ORGANISM: Artificial Sequence
111 <220> FEATURE:
112 <223> OTHER INFORMATION: Porcine (Sus scrofa) TGF-beta1/N-terminal FLAG Fusion
Construct
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116 <221> NAME/KEY: CDS
117 <222> LOCATION: (1)..(1197)
118 <223> OTHER INFORMATION: Protein coding sequence
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121 <221> NAME/KEY: misc_feature
122 <222> LOCATION: (278)..(279)
123 <223> OTHER INFORMATION: Maturation cleavage site (relates to amino acid residue
nos.)
125 <400> SEQUENCE: 8
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128 1               5                   10                  15
130 tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc gga ctg tcc acc       96
131 Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
132                 20                  25                  30
134 tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc atc gag gcc      144
135 Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
136             35                  40                  45
138 att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc ccc ccg agc      192
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139 Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
140     50                  55                  60
142 cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta ctg gct ctt     240
143 Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
144 65                  70                  75                  80
146 tac aac agt acc cgc gac cgg gta gcc ggg gaa agt gtc gaa ccg gag     288
147 Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
148                 85                  90                  95
150 ccc gag cca gag gcg gac tac tac gcc aag gag gtc acc cgc gtg cta     336
151 Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
152                 100                 105                 110
154 atg gtg gaa agc ggc aac caa atc tat gat aaa ttc aag ggc acc ccc     384
155 Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
156         115                 120                 125
158 cac agc tta tat atg ctg ttc aac acg tcg gag ctc cgg gaa gcg gtg     432
159 His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
160     130                 135                 140
162 ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc ctg ctg agg ctc     480
163 Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
164 145                 150                 155                 160
166 aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa tac agc aat     528
167 Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
168             ·    165                 170                 175
170 gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc ccc agt gac tca     576
171 Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
172             180                 185                 190
174 ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cgg cag tgg ctg     624
175 Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
176             195                 200                 205
178 acc cgc aga gag gct ata gag ggt ttt cgc ctc agt gcc cac tct tcc     672
179 Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
180     210                 215                 220
182 tct gac agc aaa gat aac aca ctc cac gtg gaa att aac ggg ttc aat     720
183 Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
184 225                 230                 235                 240
186 tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc atg aac cgg ccc     768
187 Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
188             245                 250                 255
190 ttc ctg ctc ctc atg gcc acc ccg ctg gag agg gcc cag cac ctg cac     816
191 Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
192             260                 265                 270
194 agc tcc cgg cac cgc cga gac tac aag gat gac gac gac aag gcc ctg     864
195 Ser Ser Arg His Arg Arg Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu
196             275                 280                 285
198 gat acc aac tac tgc ttc agc tcc acg gag aag aac tgc tgc gtg cgg     912
199 Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg
200     290                 295                 300
202 cag ctc tac att gac ttc cgg aag gac ctg ggc tgg aag tgg att cat     960
203 Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His
```

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204 305                      310                      315                      320
206 gaa ccc aag ggc tac cat gcc aat ttc tgc ctg ggg ccc tgt ccc tac        1008
207 Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
208              325                      330                      335
210 atc tgg agc cta gac act cag tac agc aag gtc ctg gct ctg tac aac        1056
211 Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
212              340                      345                      350
214 cag cac aac ccg ggc gcg tcg gcg gcg ccg tgc tgc gtg ccg cag gcg        1104
215 Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
216              355                      360                      365
218 ctg gag cca ctg ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg        1152
219 Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
220      370                      375                      380
222 gag cag ctg tcc aac atg atc gtg cgt tcc tgc aag tgc agc tga        1197
223 Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
224 385                      390                      395
227 <210> SEQ ID NO: 9
228 <211> LENGTH: 398
229 <212> TYPE: PRT
230 <213> ORGANISM: Artificial Sequence
232 <220> FEATURE:
233 <223> OTHER INFORMATION: Porcine (Sus scrofa) TGF-beta1/N-terminal FLAG Fusion
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242              20                      25                      30
245 Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
246              35                      40                      45
249 Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
250      50                      55                      60
253 Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
254 65                      70                      75                      80
257 Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
258              85                      90                      95
261 Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
262              100                     105                     110
265 Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
266              115                     120                     125
269 His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
270      130                     135                     140
273 Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
274 145                     150                     155                     160
277 Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
278              165                     170                     175
281 Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
282              180                     185                     190
285 Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
286              195                     200                     205
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289 Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
290     210                 215                 220
293 Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
294 225                 230                 235                 240
297 Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
298                 245                 250                 255
301 Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
302             260                 265                 270
305 Ser Ser Arg His Arg Arg Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu
306             275                 280                 285
309 Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg
310         290                 295                 300
313 Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His
314 305                 310                 315                 320
317 Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
318                 325                 330                 335
321 Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
322             340                 345                 350
325 Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
326         355                 360                 365
329 Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
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350 attcatgaac ccaagggcta ccatgccaat ttctgcctgg ggccctgtcc ctacatctgg    180
352 agcctagaca ctcagtacag caaggtcctg gctctgtaca accagcacaa cccgggcgcg    240
354 tcggcggcgc cgtgctgcgt gccgcaggcg ctggagccac tgcccatcgt gtactacgtg    300
356 ggccgcaagc ccaaggtgga gcagctgtcc aacatgatcg tgcgttcctg caagtgcagc    360
358 tga                                                                  363
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362 <211> LENGTH: 120
363 <212> TYPE: PRT
364 <213> ORGANISM: Artificial Sequence
366 <220> FEATURE:
367 <223> OTHER INFORMATION: Porcine (Sus scrofa) TGF-beta1/N-terminal FLAG Fusion
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370 <220> FEATURE:
371 <221> NAME/KEY: PEPTIDE
372 <222> LOCATION: (1)..(8)
373 <223> OTHER INFORMATION: FLAG tag
375 <400> SEQUENCE: 11
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VERIFICATION SUMMARY   DATE: 04/02/2003
PATENT APPLICATION: **US/10/017,372E**   TIME: 12:41:46

Input Set : **A:\61302 Seq Listing.txt**
Output Set: **N:\CRF4\04022003\J017372E.raw**